

SEQUENCE LISTING

<110> Chambon, Pierre - Metzger, Daniel

<120> Transgenic mouse for targeted recombination mediated by modified Cre-ER

<130> D18961

<150> FR 00 12 570

<151> 2000-10-03

<160> 14

<170> PatentIn Ver. 2.1

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<211> 1788

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(1788)

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Pro Ala Val Tyr Asn Tyr Pro Glu Gly Ala Ala Tyr Glu Phe Asn Ala
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gcg gcc gcc gcc aac gcg cag gtc tac ggt cag acc ggc ctc ccc tac 240
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Gly Pro Gly Ser Glu Ala Ala Phe Gly Ser Asn Gly Leu Gly Gly
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ttc ccc cca ctc aac agc gtg tct ccg agc ccg ctg atg cta ctg cac 336
Phe Pro Pro Leu Asn Ser Val Ser Pro Ser Pro Leu Met Leu Leu His
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Pro Pro Pro Gln Leu Ser Pro Phe Leu Gln Pro His Gly Gln Gln Val
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ccc tac tac ctg gag aac gag ccc agc ggc tac acg gtg cgc gag gcc 432
Pro Tyr Tyr Leu Glu Asn Glu Pro Ser Gly Tyr Thr Val Arg Glu Ala
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 Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe
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gat ggg gag ggc agg ggt gaa gtg ggg tct gct gga gac atg aga gct 864
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gcc aac ctt tgg cca agc ccg ctg atg atc aaa cgc tct aag aag aac 912
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3

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Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr	
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Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu	
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cat tcc ttg caa aag tat tac atc acg ggg gag gca gag ggt ttc cct	1776
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Ala Ala Ala Ala Asn Ala Gln Val Tyr Gly Gln Thr Gly Leu Pro Tyr
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Gly Pro Pro Ala Phe Tyr Arg Pro Asn Ser Asp Asn Arg Arg Gln Gly
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Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys Asn
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Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu
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5

Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro
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 Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Val
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 Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Leu
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 Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro Gly
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 Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser
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 Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys Leu
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<212> DNA

<213> Artificial sequence

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Tyr	Gly	Ala	Lys	Asp	Asp	Ser	Gly	Gln	Arg	Tyr	Leu	Ala	Trp	Ser	Gly	
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His	Ser	Ala	Arg	Val	Gly	Ala	Ala	Arg	Asp	Met	Ala	Arg	Ala	Gly	Val	
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Val	Met	Asn	Tyr	Ile	Arg	Asn	Leu	Asp	Ser	Glu	Thr	Gly	Ala	Met	Val	
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cgc	ctg	ctg	gaa	gat	ggc	gat	ctc	gag	cca	tct	gct	gga	gac	atg	aga	1056
Arg	Leu	Leu	Glu	Asp	Gly	Asp	Leu	Glu	Pro	Ser	Ala	Gly	Asp	Met	Arg	
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Ala	Ala	Asn	Leu	Trp	Pro	Ser	Pro	Leu	Met	Ile	Lys	Arg	Ser	Lys	Lys	
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Asn	Ser	Leu	Ala	Leu	Ser	Leu	Thr	Ala	Asp	Gln	Met	Val	Ser	Ala	Leu	
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Pro	Phe	Ser	Glu	Ala	Ser	Met	Met	Gly	Leu	Leu	Thr	Asn	Leu	Ala	Asp	
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agg	gag	ctg	gtt	cac	atg	atc	aac	tgg	gcg	aag	agg	gtg	cca	ggc	ttt	1296
Arg	Glu	Leu	Val	His	Met	Ile	Asn	Trp	Ala	Lys	Arg	Val	Pro	Gly	Phe	
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Val	Asp	Leu	Thr	Leu	His	Asp	Gln	Val	His	Leu	Leu	Glu	Cys	Ala	Trp	
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Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr			
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tca tct cgg ttc cgc atg atg aat ctg cag gga gag gag ttt gtg tgc			1536
Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys			
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Ser Thr Leu Lys Ser Leu Glu Lys Asp His Ile His Arg Val Leu			
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<213> Artificial sequence

<223> Chimeric sequence Homosapiens-Bacteriophage P1

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Arg	Gly	Leu	Ala	Val	Lys	Thr	Ile	Gln	Gln	His	Leu	Gly	Gln	Leu	Asn
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 Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys
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 Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr
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 Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu
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 Ser His Ile Arg His Met Ser Asn Lys Arg Met Glu His Leu Tyr Ser
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 Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met
 595 600 605
 Leu Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser
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 Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser
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 Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe

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<213> Artificial sequence

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20 25 30

gat cgc cag gcg ttt tct gag cat acc tgg aaa atg ctt ctg tcc gtt 144
Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
35 40 45

lgc cgg tcg tgg gcg gca tgg tgc aag ttg aat aac cgg aaa tgg ttt 192
Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
50 55 60

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65 70 75 80

cgc ggt ctg gca gta aaa act atc cag caa cat ttg ggc cag cta aac 288
Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
85 90 95

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Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
100 105 110

gtt tca ctg gtt atg cgg cgg atc cga aaa gaa aac gtt gat gcc ggt 384
Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
115 120 125

gaa cgt gca aaa cag gct cta gcg ttc gaa cgc act gat ttc gac cag 432
Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
130 135 140

gtt cgt tca ctc atg gaa aat agc gat cgc tgc cag gat ata cgt aat 480
Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145 150 155 160

ctg gca ttt ctg ggg att gct tat aac acc ctg tta cgt ata gcc gaa 528

12

Leu Ala Phe	Leu Gly	Ile Ala Tyr Asn Thr	Leu Leu Arg	Ile Ala Glu	
	165		170	175	
att gcc agg atc agg gtt aaa gat atc tca cgt act gac ggt ggg aga	576				
Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg					
	180		185	190	
atg tta atc cat att ggc aga acg aaa acg ctg gtt agc acc gca ggt	624				
Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly					
	195		200	205	
gta gag aag gca ctt agc ctg ggg gta act aaa ctg gtc gag cga tgg	672				
Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp					
	210		215	220	
att tcc gtc tct ggt gta gct gat gat cgg aat aac tac ctg ttt tgc	720				
Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys					
	225		230	235	240
cgg gtc aga aaa aat ggt gtt gcc gcg cca tct gcc acc agc cag cta	768				
Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu					
	245		250	255	
tca act cgc gcc ctg gaa ggg att ttt gaa gca act cat cga ttg att	816				
Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile					
	260		265	270	
tac ggc gct aag gat gac tct ggt cag aga tac ctg gcc tgg tct gga	864				
Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly					
	275		280	285	
cac agt gcc cgt gtc gga gcc gcg cga gat atg gcc cgc gct gga gtt	912				
His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val					
	290		295	300	
tca ata ccg gag atc atg caa gct ggt ggc tgg acc aat gta aat att	960				
Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile					
	305		310	315	320
gtc atg aac tat atc cgt aac ctg gat agt gaa aca ggg gca atg gtg	1008				
Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val					
	325		330	335	
cgc ctg ctg gaa gat ggc gat ctc gag cca tct gct gga gac atg aga	1056				
Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg					
	340		345	350	
gct gcc aac ctt tgg cca agc ccg ctc atg atc aaa cgc tct aag aag	1104				
Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys					
	355		360	365	
aac agc ctg gcc ttg tcc ctg acg gcc gac cag atg gtc agt gcc ttg	1152				
Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu					
	370		375	380	
ttg gat gct gag ccc ccc ata ctc tat tcc gag tat gat cct acc aga	1200				
Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg					
	385		390	395	400
ccc ttc agt gaa gct tcc atg atg ggc tta ctg acc aac ctg gca gac	1248				
Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp					

405										410					415					
agg	gag	ctg	gtt	cac	atg	atc	aac	tgg	gcg	aag	agg	gtg	cca	ggc	ttt		1296			
Arg	Glu	Leu	Val	His	Met	Ile	Asn	Trp	Ala	Lys	Arg	Val	Pro	Gly	Phe					
420										425					430					
gtg	gat	ttg	acc	ctc	cat	gat	cag	gtc	cac	ctt	cta	gaa	tgt	gcc	ttg		1344			
Val	Asp	Leu	Thr	Leu	His	Asp	Gln	Val	His	Leu	Leu	Glu	Cys	Ala	Trp					
435										440					445					
cta	gag	atc	ctg	atg	att	ggt	ctc	gtc	tgg	cgc	tcc	atg	gag	cac	cca		1392			
Leu	Glu	Ile	Leu	Met	Ile	Gly	Leu	Val	Trp	Arg	Ser	Met	Glu	His	Pro					
450										455					460					
gtg	aag	cta	ctg	ttt	gct	cct	aac	ttg	ctc	ttg	gac	agg	aac	cag	gga		1440			
Val	Lys	Leu	Leu	Phe	Ala	Pro	Asn	Leu	Leu	Leu	Asp	Arg	Asn	Gln	Gly					
465										470					475					480
aaa	tgt	gta	gag	ggc	atg	gtg	gag	atc	ttc	gac	atg	ctg	ctg	gct	aca		1488			
Lys	Cys	Val	Glu	Gly	Met	Val	Glu	Ile	Phe	Asp	Met	Leu	Leu	Ala	Thr					
485										490					495					
tca	tct	cgg	ttc	cgc	atg	atg	aat	ctg	cag	gga	gag	gag	ttt	gtg	tgc		1536			
Ser	Ser	Arg	Phe	Arg	Met	Met	Asn	Leu	Gln	Gly	Glu	Glu	Phe	Val	Cys					
500										505					510					
ctc	aaa	tct	att	att	ttg	ctt	aat	tct	gga	gtg	tac	aca	ttt	ctg	tcc		1584			
Leu	Lys	Ser	Ile	Ile	Leu	Leu	Asn	Ser	Gly	Val	Tyr	Thr	Phe	Leu	Ser					
515										520					525					
agc	acc	ctg	aag	tct	ctg	gaa	gag	aag	gac	cat	atc	cac	cga	gtc	ctg		1632			
Ser	Thr	Leu	Lys	Ser	Leu	Glu	Glu	Lys	Asp	His	Ile	His	Arg	Val	Leu					
530										535					540					
gac	aag	atc	aca	gac	act	ttg	atc	cac	ctg	atg	gcc	aag	gca	ggc	ctg		1680			
Asp	Lys	Ile	Thr	Asp	Thr	Leu	Ile	His	Leu	Met	Ala	Lys	Ala	Gly	Leu					
545										550					555					560
acc	ctg	cag	cag	cag	cac	cag	cgg	ctg	gcc	cag	ctc	ctc	ctc	atc	ctc		1728			
Thr	Leu	Gln	Gln	Gln	His	Gln	Arg	Leu	Ala	Gln	Leu	Leu	Leu	Ile	Leu					
565										570					575					
tcc	cac	atc	agg	cac	atg	agt	aac	aaa	ggc	atg	gag	cat	ctg	tac	agc		1776			
Ser	His	Ile	Arg	His	Met	Ser	Asn	Lys	Gly	Met	Glu	His	Leu	Tyr	Ser					
580										585					590					
atg	aag	tgc	aag	aac	gtg	gtg	ccc	ctc	tat	gac	ctg	ctg	ctg	gag	gcg		1824			
Met	Lys	Cys	Lys	Asn	Val	Val	Pro	Leu	Tyr	Asp	Leu	Leu	Leu	Glu	Ala					
595										600					605					
gcg	gac	gcc	cac	cgc	cta	cat	gcg	ccc	act	agc	cgt	gga	ggg	gca	tcc		1872			
Ala	Asp	Ala	His	Arg	Leu	His	Ala	Pro	Thr	Ser	Arg	Gly	Gly	Ala	Ser					
610										615					620					
gtg	gag	gag	acg	gac	caa	agc	cac	ttg	gcc	act	gcg	ggc	tct	act	tca		1920			
Val	Glu	Glu	Thr	Asp	Gln	Ser	His	Leu	Ala	Thr	Ala	Gly	Ser	Thr	Ser					
625										630					635					640
tcg	cat	tcc	ttg	caa	aag	tat	tac	atc	acg	ggg	gag	gca	gag	ggt	ttc		1968			
Ser	His	Ser	Leu	Gln	Lys	Tyr	Tyr	Ile	Thr	Gly	Glu	Ala	Glu	Gly	Phe					
645										650					655					

14

cct gcc aca gct tga
Pro Ala Thr Ala
660

1983

<210> 6
<211> 660
<212> PRT
<213> Artificial sequence
<223> Chimeric sequence Homosapiens-Bacteriophage P1

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Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
20 25 30
Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
35 40 45
Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
50 55 60
Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
65 70 75 80
Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
85 90 95
Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
100 105 110
Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
115 120 125
Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
130 135 140
Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145 150 155 160
Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
165 170 175
Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
180 185 190
Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
195 200 205
Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
210 215 220
Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225 230 235 240
Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
245 250 255

15

Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile
 260 265 270
 Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
 275 280 285
 His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
 290 295 300
 Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
 305 310 315 320
 Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
 325 330 335
 Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg
 340 345 350
 Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys
 355 360 365
 Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu
 370 375 380
 Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg
 385 390 395 400
 Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp
 405 410 415
 Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe
 420 425 430
 Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp
 435 440 445
 Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro
 450 455 460
 Val Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly
 465 470 475 480
 Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr
 485 490 495
 Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys
 500 505 510
 Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser
 515 520 525
 Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu
 530 535 540
 Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu
 545 550 555 560
 Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu
 565 570 575
 Ser His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser

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1				5					10					15			
gat	gca	acg	agt	gat	gag	gtt	cgc	aag	aac	ctg	atg	gac	atg	ttc	agg	96	
Asp	Ala	Thr	Ser	Asp	Glu	Val	Arg	Lys	Asn	Leu	Met	Asp	Met	Phe	Arg		
			20					25					30				
gat	cgc	cag	gcg	ttt	tct	gag	cat	acc	tgg	aaa	atg	ctt	ctg	ccc	gtt	144	
Asp	Arg	Gln	Ala	Phe	Ser	Glu	His	Thr	Trp	Lys	Met	Leu	Leu	Ser	Val		
			35				40						45				
tgc	cgg	tcg	tgg	gcg	gca	tgg	tgc	aag	ttg	aat	aac	cgg	aaa	tgg	ttt	192	
Cys	Arg	Ser	Trp	Ala	Ala	Trp	Cys	Lys	Leu	Asn	Asn	Arg	Lys	Trp	Phe		
	50					55					60						
ccc	gca	gaa	cct	gaa	gat	gtt	cgc	gat	tat	ctt	cta	tat	ctt	cag	gcg	240	
Pro	Ala	Glu	Pro	Glu	Asp	Val	Arg	Asp	Tyr	Leu	Leu	Tyr	Leu	Gln	Ala		
65					70					75					80		
cgc	ggt	ctg	gca	gta	aaa	act	atc	cag	caa	cat	ttg	ggc	cag	cta	aac	288	
Arg	Gly	Leu	Ala	Val	Lys	Thr	Ile	Gln	Gln	His	Leu	Gly	Gln	Leu	Asn		
				85					90					95			
atg	ctt	cat	cgt	cgg	tcg	ggg	ctg	cca	cga	cca	agt	gac	agc	aat	gct	336	
Met	Leu	His	Arg	Arg	Ser	Gly	Leu	Pro	Arg	Pro	Ser	Asp	Ser	Asn	Ala		
			100					105					110				
gtt	tca	ctg	gtt	atg	cgg	cgg	atc	cga	aaa	gaa	aac	gtt	gat	gcc	ggg	384	

Val	Ser	Leu	Val	Met	Arg	Arg	Ile	Arg	Lys	Glu	Asn	Val	Asp	Ala	Gly	
		115					120				125					
gaa	cgt	gca	aaa	cag	gct	cta	gcg	ttc	gaa	cgc	act	gat	ttc	gac	cag	432
Glu	Arg	Ala	Lys	Gln	Ala	Leu	Ala	Phe	Glu	Arg	Thr	Asp	Phe	Asp	Gln	
		130				135				140						
gtt	cgt	tca	ctc	atg	gaa	aat	agc	gat	cgc	tgc	cag	gat	ata	cgt	aat	480
Val	Arg	Ser	Leu	Met	Glu	Asn	Ser	Asp	Arg	Cys	Gln	Asp	Ile	Arg	Asn	
		145			150					155					160	
ctg	gca	ttt	ctg	ggg	att	gct	tat	aac	acc	ctg	tta	cgt	ata	gcc	gaa	528
Leu	Ala	Phe	Leu	Gly	Ile	Ala	Tyr	Asn	Thr	Leu	Leu	Arg	Ile	Ala	Glu	
			165						170					175		
att	gcc	agg	atc	agg	gtt	aaa	gat	atc	tca	cgt	act	gac	ggt	ggg	aga	576
Ile	Ala	Arg	Ile	Arg	Val	Lys	Asp	Ile	Ser	Arg	Thr	Asp	Gly	Gly	Arg	
		180						185					190			
atg	tta	atc	cat	att	ggc	aga	acg	aaa	acg	ctg	gtt	agc	acc	gca	ggt	624
Met	Leu	Ile	His	Ile	Gly	Arg	Thr	Lys	Thr	Leu	Val	Ser	Thr	Ala	Gly	
		195				200					205					
gta	gag	aag	gca	ctt	agc	ctg	ggg	gta	act	aaa	ctg	gtc	gag	cga	tgg	672
Val	Glu	Lys	Ala	Leu	Ser	Leu	Gly	Val	Thr	Lys	Leu	Val	Glu	Arg	Trp	
		210				215					220					
att	tcc	gtc	tct	ggg	gta	gct	gat	gat	ccg	aat	aac	tac	ctg	ttt	tgc	720
Ile	Ser	Val	Ser	Gly	Val	Ala	Asp	Asp	Pro	Asn	Asn	Tyr	Leu	Phe	Cys	
		225			230					235					240	
cgg	gtc	aga	aaa	aat	ggg	gtt	gcc	gcg	cca	tct	gcc	acc	agc	cag	cta	768
Arg	Val	Arg	Lys	Asn	Gly	Val	Ala	Ala	Pro	Ser	Ala	Thr	Ser	Gln	Leu	
			245						250					255		
tca	act	cgc	gcc	ctg	gaa	ggg	att	ttt	gaa	gca	act	cat	cga	ttg	att	816
Ser	Thr	Arg	Ala	Leu	Glu	Gly	Ile	Phe	Glu	Ala	Thr	His	Arg	Leu	Ile	
			260					265					270			
tac	ggc	gct	aag	gat	gac	tct	ggt	cag	aga	tac	ctg	gcc	tgg	tct	gga	864
Tyr	Gly	Ala	Lys	Asp	Asp	Ser	Gly	Gln	Arg	Tyr	Leu	Ala	Trp	Ser	Gly	
		275					280					285				
cac	agt	gcc	cgt	gtc	gga	gcc	gcg	cga	gat	atg	gcc	cgc	gct	gga	gtt	912
His	Ser	Ala	Arg	Val	Gly	Ala	Ala	Arg	Asp	Met	Ala	Arg	Ala	Gly	Val	
		290				295					300					
tca	ata	cog	gag	atc	atg	caa	gct	ggg	ggc	tgg	acc	aat	gta	aat	att	960
Ser	Ile	Pro	Glu	Ile	Met	Gln	Ala	Gly	Gly	Trp	Thr	Asn	Val	Asn	Ile	
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gtc	atg	aac	tat	atc	cgt	aac	ctg	gat	agt	gaa	aca	ggg	gca	atg	gtg	1008
Val	Met	Asn	Tyr	Ile</												

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aac agc ctg gcc ttg tcc ctg acg gcc gac cag atg gtc agt gcc ttg Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu 370 375 380			1152
ttg gat gct gag ccc ccc ata ctc tat tcc gag tat gat cct acc aga Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg 385 390 395 400			1200
ccc ttc agt gaa gct tcc atg atg gcc tta ctg acc aac ctg gca gac Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp 405 410 415			1248
agg gag ctg gtt cac atg atc aac tgg gcg aag agg gtg cca gcc ttt Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe 420 425 430			1296
gtg gat ttg acc ctc cat gat cag gtc cac ctt cta gaa tgt gcc tgg Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp 435 440 445			1344
cta gag atc ctg atg att ggt ctc gtc tgg cgc tcc atg gag cac cca Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro 450 455 460			1392
ggg aag cta ctg ttt gct cct aac ttg ctc ttg gac agg aac cag gga Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly 465 470 475 480			1440
aaa tgt gta gag gcc atg gtg gag atc ttc gac atg ctg ctg gct aca Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr 485 490 495			1488
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ctc aaa tct att att ttg ctt aat tct gga gtg tac aca ttt ctg tcc Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser 515 520 525			1584
agc acc ctg aag tct ctg gaa gag aag gac cat atc cac cga gtc ctg Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu 530 535 540			1632
gac aag atc aca gac act ttg atc cac ctg atg gcc aag gca gcc ctg Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu 545 550 555 560			1680
acc ctg cag cag cag cac cag cgg ctg gcc cag ctc ctc ctc atc ctc Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu 565 570 575			1728
tcc cac atc agg cac atg agt aac aaa gcc atg gag cat ctg tac agc Ser His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser 580 585 590			1776
atg aag tgc aag aac gtg gtg ccc ctc tat gac ctg ctg ctg gag gcg Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Ala 595 600 605			1824

19

gcg gac gcc cac cgc cta cat gcg ccc act agc cgt gga ggg gca tcc 1872
 Ala Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser
 610 615 620

gtg gag gag acg gac caa agc cac ttg gcc act gcg ggc tct act tca 1920
 Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser
 625 630 635 640

tcg cat tcc ttg caa aag tat tac atc acg ggg gag gca gag ggt ttc 1968
 Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe
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cct gcc aca gct tga 1983
 Pro Ala Thr Ala
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<210> 8

<211> 660

<212> PRT

<213> Artificial sequence

<223> Chimoric sequence Homosapiens-Bacteriophage P1

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Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
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Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
 35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
 50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
 65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
 85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
 100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
 115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
 130 135 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
 145 150 155 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
 165 170 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
 180 185 190

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Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
195 200 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
210 215 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225 230 235 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
245 250 255

Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile
260 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
290 295 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
325 330 335

Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg
340 345 350

Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys
355 360 365

Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu
370 375 380

Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg
385 390 395 400

Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp
405 410 415

Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe
420 425 430

Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp
435 440 445

Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro
450 455 460

Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly
465 470 475 480

Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr
485 490 495

Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys
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37

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